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## SEQUENCE LISTING

&lt;110&gt; Monash University

&lt;120&gt; Novel Therapeutic Molecules and Uses Therefor

&lt;130&gt; JMS/TDO/dk

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 15

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; mammalian

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (110) .. (874)

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ctg atg tcg tgg act gat ctg ttc agc aat gaa gag tac tac cct gcc 214

Leu Met Ser Trp Thr Asp Leu Phe Ser Asn Glu Glu Tyr Tyr Pro Ala

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Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser Val His Pro

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gaa tac tgg act aag cgc cat gtg tgg gag tgg ctc cag ttc tgc tgc 310

Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln Phe Cys Cys

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gac cag tac aag ttg gac acc aat tgc atc tcc ttc tgc aac ttc aac 358  
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 70 75 80

atc agt ggc ctg cag ctg tgc agc atg aca cag gag gag ttc gtc gag 406  
 Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu Phe Val Glu  
 85 90 95

gca gct ggc ctc tgc ggc gag tac ctg tac ttc atc ctc cag aac atc 454  
 Ala Ala Gly Leu Cys Gly Glu Tyr Leu Tyr Phe Ile Leu Gln Asn Ile  
 100 105 110 115

cgc aca caa ggt tac tcc ttt ttt aat gac gct gaa gaa agc aag gcc 502  
 Arg Thr Gln Gly Tyr Ser Phe Phe Asn Asp Ala Glu Glu Ser Lys Ala  
 120 125 130

acc atc aaa gac tat gct gat tcc aac tgc ttg aaa aca agt ggc atc 550  
 Thr Ile Lys Asp Tyr Ala Asp Ser Asn Cys Leu Lys Thr Ser Gly Ile  
 135 140 145

aaa agt caa gac tgt cac agt cat agt aga aca agc ctc caa agt tct 598  
 Lys Ser Gln Asp Cys His Ser His Ser Arg Thr Ser Leu Gln Ser Ser  
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cat cta tgg gaa ttt gta cga gac ctg ctt cta tct cct gaa gaa aac 646  
 His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser Pro Glu Glu Asn  
 165 170 175

tgt ggc att ctg gaa tgg gaa gat agg gaa caa gga att ttt cgg gtg 694  
 Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile Phe Arg Val  
 180 185 190 195

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 215 220 225

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 Lys Thr Gly Ile Leu Glu Arg Val Asp Arg Arg Leu Val Tyr Lys Phe  
 230 235 240

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Tyr Pro Ala Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser  
 35 40 45

Val His Pro Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln  
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Phe Cys Cys Asp Gln Tyr Lys Leu Asp Thr Asn Cys Ile Ser Phe Cys  
 65 70 75 80

Asn Phe Asn Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu  
 85 90 95

Phe Val Glu Ala Ala Gly Leu Cys Gly Glu Tyr Leu Tyr Phe Ile Leu  
 100 105 110

Gln Asn Ile Arg Thr Gln Gly Tyr Ser Phe Phe Asn Asp Ala Glu Glu  
 115 120 125

Ser Lys Ala Thr Ile Lys Asp Tyr Ala Asp Ser Asn Cys Leu Lys Thr  
 130 135 140

Ser Gly Ile Lys Ser Gln Asp Cys His Ser His Ser Arg Thr Ser Leu  
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Gln Ser Ser His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser Pro  
 165 170 175

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- 4 -

Glu Glu Asn Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile  
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Phe Arg Val Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln Arg  
 195 200 205

Lys Lys Asn Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu Arg  
 210 215 220

Tyr Tyr Tyr Lys Thr Gly Ile Leu Glu Arg Val Asp Arg Arg Leu Val  
 225 230 235 240

Tyr Lys Phe Gly Lys Asn Ala His Gly Trp Gln Glu Asp Lys Leu  
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&lt;211&gt; 637

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (134)..(613)

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tgccctcacg gta atg ttg gac tcg gtg aca cac agc acc ttc ctg cct 169

Met Leu Asp Ser Val Thr His Ser Thr Phe Leu Pro

1

5

10

aat gca tcc ctg tgc gat ccc ctg atg tcg tgg act gat ctg ttc agc 217

Asn Ala Ser Leu Cys Asp Pro Leu Met Ser Trp Thr Asp Leu Phe Ser

15

20

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aat gaa gag tac tac cct gcc ttt gag cat cag aca gat gct gat tcc 265

Asn Glu Glu Tyr Tyr Pro Ala Phe Glu His Gln Thr Asp Ala Asp Ser

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aac tgc ttg aaa aca agt ggc atc aaa agc caa gac tgt cac agt cat 313

Asn Cys Leu Lys Thr Ser Gly Ile Lys Ser Gln Asp Cys His Ser His

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T02E30" E4098/60

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                     80                                    85                                    90

agg gaa caa gga att ttt cgg gtg gtt aaa tcg gaa gcc ctg gca aag 457  
 Arg Glu Gln Gly Ile Phe Arg Val Val Lys Ser Glu Ala Leu Ala Lys  
                     95                                    100                                    105

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 Met Trp Gly Gln Arg Lys Lys Asn Asp Arg Met Thr Tyr Glu Lys Leu  
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 Ser Arg Ala Leu Arg Tyr Tyr Tyr Lys Thr Gly Ile Leu Glu Arg Val  
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gac cga agg tta gtg tac aaa ttt gga aaa aat gca cac ggg tgg cag 601  
 Asp Arg Arg Leu Val Tyr Lys Phe Gly Lys Asn Ala His Gly Trp Gln  
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&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; mammalian

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                     20                                    25                                    30

Tyr Pro Ala Phe Glu His Gln Thr Asp Ala Asp Ser Asn Cys Leu Lys  
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Thr Ser Gly Ile Lys Ser Gln Asp Cys His Ser His Ser Arg Thr Ser  
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- 6 -

Leu Gln Ser Ser His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser  
65 70 75 80

Pro Glu Glu Asn Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly  
85 90 95

Ile Phe Arg Val Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln  
100 105 110

Arg Lys Lys Asn Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu  
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- 7 -

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- 8 -

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&lt;211&gt; 1528

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&lt;220&gt;

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&lt;222&gt; (117) .. (875)

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gac ccc ctg atg cct tgg acc gat ctg ttc agc aat gaa gac tac tac 215  
 Asp Pro Leu Met Pro Trp Thr Asp Leu Phe Ser Asn Glu Asp Tyr Tyr  
 20 25 30

cct gcc ttt gag cat cag aca gcc tgt gat tcc tac tgg aca tca gtg 263  
 Pro Ala Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser Val  
 35 40 45

cac cct gaa tac tgg acc aag cgc cat gtc tgg gaa tgg ctc caa ttc 311  
 His Pro Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln Phe  
 50 55 60 65

tgc tgt gac cag tac aag ctt gat gcc aac tgc atc tcc ttc tgt cac 359  
 Cys Cys Asp Gln Tyr Lys Leu Asp Ala Asn Cys Ile Ser Phe Cys His  
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- 9 -

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Phe Asn Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu Phe	
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att gag gca gcc ggc atc tgt ggg gag tac ctg tac ttc att ctc cag	455
Ile Glu Ala Ala Gly Ile Cys Gly Glu Tyr Leu Tyr Phe Ile Leu Gln	
100 105 110	
aac att cgc tcg caa ggt tac tcc ttt ttc aat gat gct gaa gag acc	503
Asn Ile Arg Ser Gln Gly Tyr Ser Phe Phe Asn Asp Ala Glu Glu Thr	
115 120 125	
aag act ggc atc aaa gac tat gct gat tcc agt tgc ttg aaa aca agt	551
Lys Thr Gly Ile Lys Asp Tyr Ala Asp Ser Ser Cys Leu Lys Thr Ser	
130 135 140 145	
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Gly Ile Lys Ser Gln Asp Cys His Ser Arg Thr Ser Leu Gln Ser Ser	
150 155 160	
cac ctg tgg gaa ttt gtc aga gac ttg ctg ctg tcc cct gaa gag aac	647
His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser Pro Glu Glu Asn	
165 170 175	
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Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile Phe Arg Val	
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Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln Arg Lys Lys Asn	
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Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr	
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aaa acg aga att ctg gag cgg gtt gac cgg agg tta gtg tac aaa ttt	839
Lys Thr Arg Ile Leu Glu Arg Val Asp Arg Arg Leu Val Tyr Lys Phe	
230 235 240	
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Gly Lys Asn Ala His Gly Trp Gln Glu Glu Lys Leu	
245 250	

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&lt;211&gt; 253

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&lt;213&gt; mammalian

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Tyr Pro Ala Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser  
 35 40 45

Val His Pro Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln  
 50 55 60

Phe Cys Cys Asp Gln Tyr Lys Leu Asp Ala Asn Cys Ile Ser Phe Cys  
 65 70 75 80

His Phe Asn Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu  
 85 90 95

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Phe Ile Glu Ala Ala Gly Ile Cys Gly Glu Tyr Leu Tyr Phe Ile Leu  
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Gln Asn Ile Arg Ser Gln Gly Tyr Ser Phe Phe Asn Asp Ala Glu Glu  
 115 120 125

Thr Lys Thr Gly Ile Lys Asp Tyr Ala Asp Ser Ser Cys Leu Lys Thr  
 130 135 140

Ser Gly Ile Lys Ser Gln Asp Cys His Ser Arg Thr Ser Leu Gln Ser  
 145 150 155 160

Ser His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser Pro Glu Glu  
 165 170 175

Asn Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile Phe Arg  
 180 185 190

Val Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln Arg Lys Lys  
 195 200 205

Asn Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu Arg Tyr Tyr  
 210 215 220

Tyr Lys Thr Arg Ile Leu Glu Arg Val Asp Arg Arg Leu Val Tyr Lys  
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&lt;211&gt; 24

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27

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